

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/240,675DATE: 05/08/2000
TIME: 16:39:05

INPUT SET: S35440.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: BENOIT, Patrick
6 MEYER, Francois
7 MAGUIRE, Deborah
8 PLAVEC, Ivan
9 TOVEY, Michael G.
10
11 (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
12 RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
13 INTERFERON
14
15 (iii) NUMBER OF SEQUENCES: 4
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Foley & Lardner
19 (B) STREET: 3000 K Street, N.W., Suite 500
20 (C) CITY: Washington
21 (D) STATE: D.C.
22 (E) ZIP: 20007
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER: 09/240,675
32 (B) FILING DATE:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US/08/307,588
36 (B) FILING DATE: 05-DEC-1994
37 (A) APPLICATION NUMBER: PCT/EP93/00770
38 (B) FILING DATE: 30-MAR-1993
39
40 (vii) PRIOR APPLICATION DATA:
41 (A) APPLICATION NUMBER: EP 92400902.0
42 (B) FILING DATE: 31-MAR-1992
43
44 (viii) ATTORNEY/AGENT INFORMATION:
45 (A) NAME: SAXE, Bernhard D.
46 (B) REGISTRATION NUMBER: 28,665

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47 (C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL
48
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: (202)672-5300
51 (B) TELEFAX: (202)672-5399
52
53 (2) INFORMATION FOR SEQ ID NO: 1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 1343 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: double
59 (D) TOPOLOGY: linear
60
61 (ii) MOLECULE TYPE: DNA (genomic)
62
63
64 (ix) FEATURE:
65 (A) NAME/KEY: CDS
66 (B) LOCATION: 27..1334
67
68
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70
71 CTGCAGGGAT CTGCGGCGGC TCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53
72 Met Met Val Val Leu Leu Gly Ala Thr
73 1 5
74
75 ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101
76 Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala
77 10 15 20 25
78
79 GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA 149
80 Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile
81 30 35 40
82
83 GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197
84 Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly
85 45 50 55
86
87 AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245
88 Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp
89 60 65 70
90
91 ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293
92 Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe
93 75 80 85
94
95 TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341
96 Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg
97 90 95 100 105
98
99 GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389

RAW SEQUENCE LISTING PATENT APPLICATION US/09/240,675

DATE: 05/08/2000
TIME: 16:39:06

INPUT SET: S35440.raw

100	Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr	
101	110 115 120	
102		
103	CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT	437
104	Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala	
105	125 130 135	
106		
107	GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT	485
108	Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser	
109	140 145 150	
110		
111	GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC	533
112	Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile	
113	155 160 165	
114		
115	TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC	581
116	Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser	
117	170 175 180 185	
118		
119	AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA	629
120	Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys	
121	190 195 200	
122		
123	GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA	677
124	Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro	
125	205 210 215	
126		
127	GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA	725
128	Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu	
129	220 225 230	
130		
131	AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT	773
132	Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp	
133	235 240 245	
134		
135	TAT ACA TAT GCA AAC ATG ACC TTT CAA GTT CAG TGG CTC CAC GCC TTT	821
136	Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe	
137	250 255 260 265	
138		
139	TTA AAA AGG AAT CCT GGA AAC CAT TTG TAT AAA TGG AAA CAA ATA CCT	869
140	Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro	
141	270 275 280	
142		
143	GAC TGT GAA AAT GTC AAA ACT ACC CAG TGT GTC TTT CCT CAA AAC GTT	917
144	Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val	
145	285 290 295	
146		
147	TTC CAA AAA GGA ATT TAC CTT CTC CGC GTA CAA GCA TCT GAT GGA AAT	965
148	Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn	
149	300 305 310	
150		
151	AAC ACA TCT TTT TGG TCT GAA GAG ATA AAG TTT GAT ACT GAA ATA CAA	1013
152	Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/240,675

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INPUT SET: S35440.raw

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153          315          320          325
154
155 GCT TTC CTA CTT CCT CCA GTC TTT AAC ATT AGA TCC CTT AGT GAT TCA      1061
156 Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser
157 330          335          340          345
158
159 TTC CAT ATC TAT ATC GGT GCT CCA AAA CAG TCT GGA AAC ACG CCT GTG      1109
160 Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val
161          350          355          360
162
163 ATC CAG GAT TAT CCA CTG ATT TAT GAA ATT ATT TTT TGG GAA AAC ACT      1157
164 Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr
165          365          370          375
166
167 TCA AAT GCT GAG AGA AAA ATT ATC GAG AAA AAA ACT GAT GTT ACA GTT      1205
168 Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val
169          380          385          390
170
171 CCT AAT TTG AAA CCA CTG ACT GTA TAT TGT GTG AAA GCC AGA GCA CAC      1253
172 Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His
173          395          400          405
174
175 ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA      1301
176 Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val
177 410          415          420          425
178
179 TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA TGAGGTACC      1343
180 Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys
181          430          435
182
183
184 (2) INFORMATION FOR SEQ ID NO: 2:
185
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 436 amino acids
188 (B) TYPE: amino acid
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: protein
192
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
194
195 Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
196 1          5          10          15
197
198 Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser
199 20          25          30
200
201 Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
202 35          40          45
203
204 Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
205 50          55          60

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/240,675

DATE: 05/08/2000
TIME: 16:39:07

INPUT SET: S35440.raw

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206
207 Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
208 65 70 75 80
209
210 Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
211 85 90 95
212
213 Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
214 100 105 110
215
216 Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
217 115 120 125
218
219 Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
220 130 135 140
221
222 His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
223 145 150 155 160
224
225 Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
226 165 170 175
227
228 Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
229 180 185 190
230
231 Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
232 195 200 205
233
234 Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
235 210 215 220
236
237 Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln
238 225 230 235 240
239
240 Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
241 245 250 255
242
243 Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
244 260 265 270
245
246 His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
247 275 280 285
248
249 Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
250 290 295 300
251
252 Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
253 305 310 315 320
254
255 Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
256 325 330 335
257
258 Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala

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PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text